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|   |     |                                       |
|---|-----|---------------------------------------|
| 1 | 59  | ASPGLU-RICH (ACIDIC).                 |
| 2 | 304 | NUCLEAR LOCALIZATION SIGNAL (POTENT   |
| 3 | 316 | NUCLEAR LOCALIZATION (BY SIMILARITY). |
| 4 | 385 | PHOSPHORYLATION (BY SIMILARITY).      |
| 5 | 380 | R -> T (IN REF. 2).                   |
| 6 | 386 | AA; 43255 MW; Q322BF3D CRG32).        |

Query Match 22.5%; Score 760.5; DB 1; Length 386;  
Best Local Similarity 44.28; Pred. No. 1.4e-43;

60 SYMAQENLLSTMDQMSSRAASAPYT-----PEHAASYPTHS-PTAQPSSTFTDM 109  
::: : ||||| ::| ||| | | : | | | | : |  
24 NLLPENNLSS---ELSAVDLLPYTDTATWLDGCPNEAQPOMPEPSAPAAPPAT---- 77

110 SPAV-----IPSNTPYPGPHFFVTFQSSSTAKSATWTYSPLLKLYCQIAKTCPI 161  
 ||| ||| : : ||| ||| ||| ||| ||| ||| :  
 77 -PAPATSWPLSSFVPSQKTPGNYGFRLGFLQSGPAKSVTCYSPSLNKLFCOLAKTCPV 135

```
162 QIKVSTPPPTAIRAMPYKKAHVTDVKRCPNHELGRDENEGQSAPASHLIRVEGNN 221  
   f- : ||||| : || : || | : || : || : || : || : || : || : || : ||  
136 QLWVDSPPPGTRVMALYKKLEHTEWRRCPHERSSDYSVG-LAPPCHLRVEGTI 194
```

222 LSQVDDPVTGRQSVVPVEPPQVGTEFTILYNFMCNSSCVGGMNRRPILIIITLEMRD 281  
:::| | | | | | | : | | | | | | | | | |  
195 RAEYDDRNTFRHSVVVPYESPEIDSECTTIHNFMCNSSCGGMNRPBTITITIFNSC 254

```

282 GOVLGRRSEFGRICACPGDRKADHDHYREQ-QALNESSAFNGAASKRAFQSPPAVPAL 340
| :||| ||| |:|||||:: ::::| :||| :|
255 GNILGRNSEFYRVCAQCDQRRTTFENIRKGQSCDEDDPDP--STKDRI DTNTSSDGO- 317

```

341 GAGVKKRRHGDETTYIQLVRGRENFEILMKLKSLELMELVPQPLVDVSFRQQQLQRPS 400  
|:: | : | :: | : | : | :: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
331 ---PKKPIQGEVETQTIGEKDYEMWERFINAYEYKAT---ADGDCGCGCAUCC 260

401 HLQP---PSYGPVLSPMNKVHG 419  
||: || || || || ||  
361 HTSKFQPDSCSCVYVMTVDSG 389

53\_SHEEP STANDARD; PRT; 382 AA.  
51664;  
1-OCT-1996 (Rel. 34, Created)

1-NOV-1997 (Rel. 35, Last annotation update)  
CELLULAR TUMOR ANTIGEN P53.  
P53.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Utheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae;  
Caprinae; Ovis.

SEQUENCE FROM N.A.  
TISSUE= BLOOD;  
MEDLINE; 95352828.  
DEQUIEDT.E., KERTMANN R., BUR. A., WILLEMS L.;  
"Nucleotide sequence of the ovine p53 tumor-suppressor cDNA and its  
genomic organization.";  
DNA SECT. 5:255-259(1995).  
-!- FUNCTION: ACT AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES  
GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL  
CIRCUMSTANCES OR CELL TYPE; BUT BOTH ACTIVITIES ARE INVOLVED IN  
TUMOR SUPPRESSION. IT ACTS IN CELL CYCLE REGULATION, IT IS A  
TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELLULAR DIVISION  
BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF  
THE GENES ACTIVATED IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES,  
APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF  
BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2  
EXPRESSION.

-1- SUBCELLULAR LOCATION: NUCLEAR.  
-1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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EMBL; X81705; CAA57349.1; -.  
HSP; P04637; IPET.  
PROSITE; PS00348; P53; 1.  
PFAM; PF00870; P53; 1.  
Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
Nuclear protein; Phosphorylation; Apoptosis.  
DOMAIN 1 66 AS/GLU-RICH (ACIDIC).  
DOMAIN 300 312 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
MOD\_RES 381 381 PHOSPHORYLATION (BY SIMILARITY).  
SEQUENCE 382 AA; 42809 MW; OCB39A00 CRC32;

|                       |              |                   |                |            |
|-----------------------|--------------|-------------------|----------------|------------|
| Query Match           | 22.3%        | Score 755.5       | DB 1           | Length 382 |
| Best Local Similarity | 44.8%        | Pred. No. 2.9e-43 |                |            |
| Matches 168           | Conservative | 62                | Mismatches 110 | Indels 35  |
|                       |              |                   |                | Gaps 10    |

60 SVMAGFNLLSSTMDQMSSRAASAPYT-----PEHAASVPTHSPVAQPSSTFDTM 109  
::: ||||| :::  
24 NLLPENNNLASS---ELSAVDDDLPLYSIEDVTWLDCEPNKPAQMP--EPQAALAPATS 78

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110 SP-APVIPNTDYGCPHHFEVTFQOSTAKSATWYSPDLLKKLXCQIAKTCPIQIKVSTP 168
      _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _ _
79 WPLSEFVQKTYPGNYGFRLGFELHSGTAKSVTCYTPSINKLFCOLAKTCPVOLWVDSP 138

```

**a**

```
169 PPCTAIRAMPVYKKAHYTDVKRCPNHUELGDFNEGGSAPASHLIRVEGNNISQYVDD 228  
||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
b 139 PPCTRTVRMAIYKKLEHTEVRRSPHRRSSDYSDG-LAPPQHLIRVEGNIRAEEYFD 197  
||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
```

**a** 229 PVTGRQSVVVVPEPPQVGTEFTTILYNFMCNCSGVGMNRRLIIITILEMRDGOVLGRR 288  
| | | | | : | | | | | : | | | | | : | | | | |  
**b** 198 RNTFRSHVVVPYSEISECTTHYNFMCNSSCGMGNRRLTIITLFDSPGNLIGRS 257  
| | | | | : | | | | | : | | | | | : | | | | |

289 SFERICACPGRRKADEDHYRQ-QALNESSAKNGAASKRAFKQSPAPVAPALGAGVKKR 347  
288  
258 SFERVACAPGRPRRTTETENRKGOSDFDDP--GGMKPAVDSSTSSSDP-----GVK 308  
257

348 RHGEDTYLQVRGRENFEILMKLESLELMELVQPPLVDSYRQQQLLRPSHLP--- 405  
 : : : : : : : : : : : : : : : : :  
 310 KPIDGEVTIIGRKRRMEFSEINFALIMO-----NOCREPCCEPASHYLSWGC 363  
 : : : : : : : : : : : : : : : : :  
 310 KPIDGEVTIIGRKRRMEFSEINFALIMO-----NOCREPCCEPASHYLSWGC 363

Y  
405 PSYGPVLSPMNKVHG 419  
|| || || ||  
364 PPSGCHUKKVVMT KPPC 378